

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 18:42:21 ; Search time: 87.3111 Seconds  
(without alignments)  
4456.258 Million cell updates/sec

Title: US-09-914-042-1  
Perfect score: 5273  
Sequence: 1 MPDQISVSEFVAETHDYKA.....DGPGRKGAFFVSVFHFIAD 1006

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04: \*  
1: Genesecp1980s: \*  
2: Genesecp1990s: \*  
3: Genesecp2000s: \*  
4: Genesecp2001s: \*  
5: Genesecp2002s: \*  
6: Genesecp2003as: \*  
7: Genesecp2003bs: \*  
8: Genesecp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5253	99.6	1006	2	Aaw77290 Human dif
2	5084	96.4	1006	3	Aab236647 Human Pap
3	3874	73.5	982	2	Aaw77288 Zebrafish
4	3710.5	70.4	783	3	Aab236648 Murine Pa
5	3155	59.8	903	2	Aaw77289 Zebrafish
6	3029	57.4	1072	7	Add71162 Human int
7	3024.5	57.4	1129	7	Add71155 Human int
8	3013.5	57.1	1129	2	Aaw77286 Bovine di
9	3011	57.1	1090	6	Aae38437 Mouse ASA
10	3006	57.0	1132	8	Adj51009 Human nov
11	3000.5	56.9	1147	6	Aae38436 Mouse ASA
12	2954.5	56.0	1151	2	Aaw77287 Zebrafish
13	2852	54.1	1087	8	Ads34461 POSH prot
14	2465.5	46.8	956	8	Ads34457 POSH prot
15	2410	45.7	949	8	Ads34458 POSH prot
16	2369	44.9	940	8	Ads10772 Human the
17	2363	44.8	940	4	Aam40068 Human pol
18	2071.5	39.3	903	7	Adb64797 Human pro
19	2071.5	39.3	903	7	Adk81947 Hepatocel
20	1801.5	34.2	350	4	Adi5432 Novel cen
21	1801.5	34.2	350	8	Adi5432 Novel cen
22	1759.5	33.4	349	8	Aau87438 Novel hum
23	1759.5	33.4	349	8	Adi54753 Novel hum
24	1695.5	32.2	1020	4	Abbs8971 Drosophil
25	1075.5	20.4	208	7	Adb64130 Human pro

26	802	15.2	459	4	AAU20370 Human sec
27	611.5	11.6	358	7	Adj71009 Human hea
28	579	11.0	407	5	Abb97460 Novel hum
29	573.5	10.9	778	7	Add71161 Human int
30	571.5	10.8	778	4	AAm39122 Human pol
31	569	10.8	407	6	ABU70671 Human adi
32	562	10.7	799	4	ABG17242 Novel hum
33	558	10.6	764	6	ABU52617 Human NOV
34	551	10.4	804	5	ABB97954 Human pro
35	532.5	10.1	805	4	AAm40908 Human pol
36	530.5	10.1	958	8	ADS10512 Human the
37	529	10.0	834	5	ABG91802 Human int
38	529	10.0	834	5	AAU99904 Human 468
39	509	9.7	740	8	ADS34455 POSH prot
40	480	9.1	156	4	ABb11268 Human dif
41	439	8.3	828	4	ABB62649 Drosophil
42	422.5	8.0	560	4	AAE07122 Human gen
43	419	7.9	605	5	ABG93808 Transcrip
44	419	7.9	605	5	AAU71799 Zinc fing
45	412	7.8	176	4	AAm41854 Human pol

ALIGNMENTS

RESULT 1  
AAW77290  
ID AAW77290 standard; protein; 1006 AA.  
XX AC  
XX AC  
XX 20-NOV-1998 (first entry)  
XX  
DE Human differentiation enhancing factor 2 gene.  
XX  
KW Human; differentiation enhancing factor; ankyrin repeat; C2 domain;  
KW SH3 consensus binding sequence; pleckstrin homology domain; adipogenesis;  
KW neurogenesis; hyperplastic disease; neoplastic disease; nervous system.  
XX  
OS Homo sapiens.  
XX  
PN WO9836065-A1.  
XX  
PD 20-AUG-1998.  
XX  
PF 13-FEB-1998; 98WO-US0002724.  
XX  
PR 14-FEB-1997; 97US-0038191P.  
XX  
PA (DAND ) DANA FARBER CANCER INST INC.  
XX  
PI Thomas RM, King FJ, Harris DF, Hu E, Spiegelman B, Chan J;  
XX  
DR WPI; 1998-467173/40.  
XX  
PT New nucleic acid encoding differentiation enhancing factor - used  
PT particularly to regulate adipogenesis and neurogenesis, e.g. for treating  
PT tumours and neurological disease.  
XX  
PS Example 13; Fig 12; 203pp; English.  
XX  
CC The differentiation enhancing factors (DEF), comprise at least one each  
CC of SH3 consensus binding sequence, ankyrin repeat, pleckstrin homology  
CC domain and C2 domain. The DEF induce adipogenesis or neurogenesis; they  
CC are mediators of SH3-domain dependent signalling and may be involved in  
CC cellular gene expression, cytoskeletal architecture, protein trafficking,  
CC endocytosis or adhesion, migration, proliferation and differentiation of  
CC cells. Typical applications of DEF and agents that modulate interaction  
CC between the protein and it's ligand, or of nucleic acid expressing them,  
CC are treatment of hyperplastic and neoplastic disease (a wide range of  
CC solid tumours and leukaemias), including metastases; for in vitro  
CC induction of differentiation of neural crest cells to neurons, glial  
CC cells etc.; for increasing neuron survival, and inducing cell repair, in

Exhibit A

CC the nervous system (e.g. treatment of traumatic injury, stroke,  
 CC Alzheimer's, Parkinson's or Huntington's diseases, amyotrophic lateral  
 CC sclerosis, multiple sclerosis etc.)  
 XX Sequence 1006 AA;

Query Match 99.6%; Score 5253; DB 2; Length 1006;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 1003; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPDQISVSEFVAETHEDYKAPTASSFTTRTAQCNRTVAALDEALDVRMVLKMKSVKA 60  
 DB 1 MPDQISVSEFVAETHEDYKAPTASSFTTRTAQCNRTVAALDEALDVRMVLKMKSVKA 60  
 QY 61 INSSGLAHVENEEOYTQALEKFGGNCVCRDDPDLSAFLKFSVFTKELTALFNLIQNMN 120  
 DB 61 INSSGLAHVENEEOYTQALEKFGGNCVCRDDPDLSAFLKFSVFTKELTALFNLIQNMN 120  
 QY 121 NIISFPDLSLLKGDVGKDLKPKDPKAWKDYETKITKLEKKEKHAHLGHMIRTEISG 180  
 DB 121 NIISFPDLSLLKGDVGKDLKPKDPKAWKDYETKITKLEKKEKHAHLGHMIRTEISG 180  
 QY 181 AETAEMEKKERRFFQLOMCEYLLKVNIEIKKGVDDLQNLKIFYHAQCNCFFDGLKAVES 240  
 DB 181 AETAEMEKKERRFFQLOMCEYLLKVNIEIKKGVDDLQNLKIFYHAQCNCFFDGLKAVES 240  
 QY 241 LKPSIETLSTDLHTTKQAQDEERRQLIQRLDILKSAQVEQKEDSQIROSTAYSILHQPQ 300  
 DB 241 LKPSIETLSTDLHTTKQAQDEERRQLIQRLDILKSAQVEQKEDSQIROSTAYSILHQPQ 300  
 QY 301 NKEHGTENGSLYKSDGIRKWKQKSVKNGFLTISHGTANRPPAKNLTLTQVKTNP 360  
 DB 301 NKEHGTENGSLYKSDGIRKWKQKSVKNGFLTISHGTANRPPAKNLTLTQVKTNP 360  
 QY 361 BEKKCFDLISHDRYHFOAEDQECQIWMVLSQNSKEALNNAFKGDDNTGENNIVBELT 420  
 DB 361 BEKKCFDLISHDRYHFOAEDQECQIWMVLSQNSKEALNNAFKGDDNTGENNIVBELT 420  
 QY 421 KEIISVORTGNDVCCGAPDPTLSTNLGILTCIECSGIIHRELGVHSPQSLDVL 480  
 DB 421 KEIISVORTGNDVCCGAPDPTLSTNLGILTCIECSGIIHRELGVHSPQSLDVL 480  
 QY 481 LGTSELLAKNIGNAGNETMECLPAEDSVKPNPGSDMNARKDYITAKVIERRYARKKH 540  
 DB 481 LGTSELLAKNIGNAGNETMECLPAEDSVKPNPGSDMNARKDYITAKVIERRYARKKH 540  
 QY 541 ADNAAKLHSLCEAVKTRDIFGLQAVAGVDLITEKIPLANGHEPDETLHLAVRSVDRTS 600  
 DB 541 ADNAAKLHSLCEAVKTRDIFGLQAVAGVDLITEKIPLANGHEPDETLHLAVRSVDRTS 600  
 QY 601 LHVDFLVQNSGNDKQTKGKSTALHYCCLTDAECLKLLRGKASIEIANESGETPLDI 660  
 DB 601 LHVDFLVQNSGNDKQTKGKSTALHYCCLTDAECLKLLRGKASIEIANESGETPLDI 660  
 QY 661 AKRLKHECEELLTQALSRFNHSHVYEWRLHEDLDESDDMDKLOPSENRDRP 720  
 DB 661 AKRLKHECEELLTQALSRFNHSHVYEWRLHEDLDESDDMDKLOPSENRDRP 720  
 QY 721 ISFYQLGNSQLQSNVSLARDAANLAKKORAFMPSILQNETYGALLSGSPPPAPAPAS 780  
 DB 721 ISFYQLGNSQLQSNVSLARDAANLAKKORAFMPSILQNETYGALLSGSPPPAPAPAS 780  
 QY 781 TTSAPPLPPRNVGKVQTASSANTLWKTNSVSDGSRSSDDPPAVHPLPLPRLVSTN 840  
 DB 781 TTSAPPLPPRNVGKVQTASSANTLWKTNSVSDGSRSSDDPPAVHPLPLPRLVSTN 840  
 QY 841 PLTPTPPPVAKTPSWEALSOPEKAPPGISQIRPPPLPPQPSRLPQKPPAGTKST 900  
 DB 841 PLTPTPPPVAKTPSWEALSOPEKAPPGISQIRPPPLPPQPSRLPQKPPAGTKST 900  
 QY 901 PLTNKQPRGPDLSATEALGPLSNAMVLQPPAPMPRKQATKLKPRVKALVNCVADNP 960  
 DB 901 PLTNKQPRGPDLSATEALGPLSNAMVLQPPAPMPRKQATKLKPRVKALVNCVADNP 960

QY 961 DELTFSEGDIIVDGEEDQEWIGHIDGDPGRKGAPFVSFVHFIAID 1006  
 DB 961 DELTFSEGDIIVDGEEDQEWIGHIDGDPGRKGAPFVSFVHFIAID 1006

## RESULT 2

AAB23647  
 ID AAB23647 standard; protein; 1006 AA.  
 XX AAB23647;  
 XX AAB23647;  
 DT 05-JAN-2001 (first entry)  
 DE Human Pap-Delta protein sequence SEQ ID NO:1.

KW Pap; Pyk2 binding protein; Pyk2 C-terminus associated protein; diagnosis;  
 KW cytostatic; neuroprotective; immunomodulatory; cardioactive; cancer;  
 KW cardiovascular disorder; neurodegenerative disorder; immune disorder.  
 XX Homo sapiens.

XX WO200049144-A2.

XX 24-AUG-2000.

XX 18-FEB-2000; 2000WO-US004647.

XX 22-FEB-1999; 99US-0121125P.

XX (SUGEN-) SUGEN INC.

XX Lev S, Schlessinger J, Chen A, Hernandez J, Martinez R;

XX Plowman GD;

XX WPI; 2000-524592/47.

XX Pyk2 binding protein nucleic acids, polypeptides, antibodies and  
 XX antisense oligonucleotides, the oligonucleotides are useful for treating  
 XX cancer or a cardiovascular, neurodegenerative or immune disorder.  
 XX Claim 15; Fig 1; 132pp; English.

XX The present sequence represents the human Pap-Delta protein. Pap is a  
 XX Pyk2 C-terminal associated protein (Pyk2 binding protein). Pap proteins  
 XX have cytosolic, neuroprotective, immunomodulatory and cardioactive  
 XX activities. Pyk2 binding protein polypeptides such as Pap are useful as  
 XX diagnostic agents for the detection of diseases. Oligonucleotides from  
 XX polynucleotide sequences encoding Pap proteins may be useful for the  
 XX treatment of diseases such as cancer or a cardiovascular,  
 XX neurodegenerative or immune disorder

XX Sequence 1006 AA;

QY Query Match 96.4%; Score 5084; DB 3; Length 1006;

DB Best Local Similarity 97.7%; Pred. No. 0;

QY Matches 983; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

DB 1 MPDQISVSEFVAETHEDYKAPTASSFTTRTAQCNRTVAALDEALDVRMVLKMKSVKA 60

QY 1 MPDQISVSEFVAETHEDYKAPTASSFTTRTAQCNRTVAALDEALDVRMVLKMKSVKA 60

DB 61 INSSGLAHVENEEOYTQALEKFGGNCVCRDDPDLSAFLKFSVFTKELTALFNLIQNMN 120

QY 61 INSSGLAHVENEEOYTQALEKFGGNCVCRDDPDLSAFLKFSVFTKELTALFNLIQNMN 120

DB 121 NIISFPDLSLLKGDVGKDLKPKDPKAWKDYETKITKLEKKEKHAHLGHMIRTEISG 180

QY 121 NIISFPDLSLLKGDVGKDLKPKDPKAWKDYETKITKLEKKEKHAHLGHMIRTEISG 180

DB 181 AETAEMEKKERRFFQLOMCEYLLKVNIEIKKGVDDLQNLKIFYHAQCNCFFDGLKAVES 240

QY 181 AETAEMEKKERRFFQLOMCEYLLKVNIEIKKGVDDLQNLKIFYHAQCNCFFDGLKAVES 240

QY 241 LKPSIETLSTDLHTI KOAQDEERRQLIQRLDILKSAQVEQKEDSQIRQSTAYSILHQPOG 300  
 Db 241 LKPSIETLSTDLHTI KOAQDEERRQLIQRLDILKSAQVEQKEDSQIRQSTAYSILHQPOG 300  
 QY 301 NKEHGTERNGSLYKKSQDGIKRVWQKRCVKNGLFTTISHGTANRPPAKJNLTLTCCOVKTNP 360  
 Db 301 NKEHGTERNGSLYKKSQDGIKRVWQKRCVKNGLFTTISHGTANRPPAKJNLTLTCCOVKTNP 360  
 QY 361 EEKCFDLISHDRTHYFQAEDEQECQIWMVSLQNSKEEALNNAFKGDDNTGENNIVQELT 420  
 Db 361 EEKCFDLISHDRTHYFQAEDEQECQIWMVSLQNSKEEALNNAFKGDDNTGENNIVQELT 420  
 QY 421 KEIITSEVORTGNDVCCDCCGAPDPTWLTNLGILTCIECSGIRHRELGVHYSRMOQLTLDV 480  
 Db 421 KEIITSEVORTGNDVCCDCCGAPDPTWLTNLGILTCIECSGIRHRELGVHYSRMOQLTLDV 480  
 QY 481 LGTSELLAKNIGNAGFNETMECCLPADSVKPNPFGSDMNAKDYITAKYIERRYARKKH 540  
 Db 481 LGTSELLAKNIGNAGFNETMECCLPADSVKPNPFGSDMNAKDYITAKYIERRYARKKH 540  
 QY 541 ADNAKLHSLCEAVKTRDIFGLLOAYADGVDLTEKIPLANGHEPDETALHLAVRSVDRTS 600  
 Db 541 ACNAKLHSLCEAVKTRDIFGLLOAYADGVDLTEKIPLANGHEPDETALHLAVRSVDRTS 600  
 QY 601 LHIVDFLVQNSGNLDKQTKGKSTALHYCCCLTDNAECLKLLRGKASIEIANESGETPLDI 660  
 Db 601 LHIVDFLVQNSGNLDKQTKGKSTALHYCCCLTDNAECLKLLRGKASIEIANESGETPLDI 660  
 QY 661 AKRLKHEHCHELLTQALSGRPNFNSHVHVEYEWRLLEDLDESDDDMDKLOPSENRRDRP 720  
 Db 661 AKRLKHEHCHELLTQALSGRPNFNSHVHVEYEWRLLEDLDESDDDMDKLOPSENRRDRP 720  
 QY 721 ISFYQLGSLNQLQNAVSLARDAANLAKEKORAFMPSILQNETYCALLSGSPPPAPAPAPS 780  
 Db 721 ISFYQLGSLNQLQNAVSLARDAANLAKEKORAFMPSILQNETYCALLSGSPPPAPAPAPS 780  
 QY 781 TTSAPPLPPNKGKVTQASSANTLWKTNSVSDGGRQRSSDPPAVHPLPLPLRVSTN 840  
 Db 781 TTSAPPLPPNKGKVTQASSANTLWKTNSVSDGGRQRSSDPPAVHPLPLPLRVSTN 840  
 QY 841 PLTPTPTPPVAKTPSVMEALSQSKPAPGSIQIRPPPLPQPSRLPQKPPAPGTDKST 900  
 Db 841 PLTPTPTPPVAKTPSVMEALSQSKPAPGSIQIRPPPLPQPSRLPQKPPAPGTDKST 900  
 QY 901 PLTKGQPRGPDLSATEALGPLSNAMVLQPPAPMPKRSQATKLPKRVKALYNCVADNP 960  
 Db 901 PLTKGQPRGPDLSATEALGPLSNAMVLQPPAPMPKRSQATKLPKRVKALYNCVADNP 960  
 QY 961 DELTFSEGDIIVDGBEDQEWIIGHIDGDPGRKAPFVSVFHIAD 1006  
 Db 961 DELTFSEGDIIVDGBEDQEWIIGHIDGDPGRKAPFVSVFHIAD 1006

RESULT 3  
 AAW77288  
 ID AAW77288 standard; protein; 982 AA.  
 XX  
 AC AAW77288;  
 XX  
 AC  
 XX  
 DT 17-OCT-2003 (revised)  
 DT 20-NOV-1998 (first entry)  
 XX  
 XX Zebrafish differentiation enhancing factor 2 protein.  
 XX Zebrafish; differentiation enhancing factor; ankyrin repeat; C2 domain;  
 KW SH3 consensus binding sequence; pleckstrin homology domain; adipogenesis;  
 KW neurogenesis; hyperplastic disease; neoplastic disease; nervous system.  
 XX  
 OS Danio rerio.  
 XX  
 XX W09836065-A1.  
 FN  
 XX

PD 20-AUG-1998.  
 XX 13-FEB-1998; 98MO-US002724.  
 XX 14-FEB-1997; 97US-0038191P.  
 PA (DAND ) DANA FARBER CANCER INST INC.  
 XX Thomas RM, King FU, Harris DF, Hu E, Spiegelman B, Chan J;  
 PI WPI; 1998-457173/40.  
 DR N-PSDB; AAVS9105.  
 XX New nucleic acid encoding differentiation enhancing factor - used  
 PT particularly to regulate adipogenesis and neurogenesis, e.g. for treating  
 PT tumours and neurological disease.  
 XX Claim 3; Fig 12; 203pp; English.  
 PS The differentiation enhancing factors (DEF), comprise at least one each  
 CC of SH3 consensus binding sequence, ankyrin repeat, pleckstrin homology  
 CC domain and C2 domain. The DEF induce adipogenesis or neurogenesis; they  
 CC are mediators of SH3-domain dependent signalling and may be involved in  
 CC cellular gene expression, cytoskeletal architecture, protein trafficking,  
 CC endocytosis or adhesion, migration, proliferation and differentiation of  
 CC cells. Typical applications of DEF and agents that modulate interaction  
 CC between the protein and it's ligand, or of nucleic acid expressing them,  
 CC are treatment of hyperplastic and neoplastic disease (a wide range of  
 CC solid tumours and leukaemias), including metastases; for in vitro  
 CC induction of differentiation of neural crest cells to neurons, glial  
 CC cells etc.; for increasing neuron survival, and inducing cell repair, in  
 CC the nervous system (e.g. treatment of traumatic injury, stroke, stroke,  
 CC Alzheimer's, Parkinson's or Huntington's diseases, amyotrophic lateral  
 CC sclerosis, multiple sclerosis etc.). (Updated on 17-OCT-2003 to  
 CC standardise OS field)  
 XX Sequence 982 AA;

Query Match 73.5%; Score 3874; DB 2; Length 982;  
 Best Local Similarity 74.1%; Pred. No. 6.4e-264;  
 Matches 755; Conservative 92; Mismatches 122; Indels 50; Gaps 13;  
 QY 1 MPDQISVSFEVTHEDYKAPTASSFTTRTAQCRNTVAATEEALVDVRLVYKMKSVKA 60  
 Db 1 MPDQITVAEFVTETNEDYKAPTASSFTTRTAQCRNTVAATEEALVDVRLVYKMKSVKA 60  
 QY 61 INSSGLAHVENEEOYTOALEKFGGNCVCRDDPDLSAFLKFSVFTKELTALFKNLQNMN 120  
 Db 61 IYASGLAHVENEEOYTOALEKFGGNCVCRDDPDLSAFLKFSVFTKELTALFKNLQNMN 120  
 QY 121 NIISPFLDLSLLKGLKGVKDLKPKDPKAWKDYETKITKEKEKHAHLGHWIRTEISG 180  
 Db 121 NIITPFLDLSLLKGLKGVKDLKPKDPKAWKDYETKITKEKEKHAHLGHWIRTEISG 180  
 QY 181 ASIASEMEKERRFFOLQMCCEYLLKVNIEIKKGVLDLQNLIKYFHAQCQNFQDGLKAVES 240  
 Db 181 ASIASEMEKERRFFOLQMCCEYLLKVNIEIKKGVLDLQNLIKYFHAQCQNFQDGLKAVDN 240  
 QY 241 LKPSIETLSTDLHTI KOAQDEERRQLIQRLDILKSAQVEQKEDSQIRQSTAYSILHQPOG 300  
 Db 241 LKPSIETLSTDLHTI KOAQDEERRQLIQRLDILKSAQVEQKEDSQIRQSTAYSILHQPOG 300  
 QY 301 NKEHGTERNGSLYKKSQDGIKRVWQKRCVKNGLFTTISHGTANRPPAKJNLTLTCCOVKTNP 360  
 Db 301 NKEHGTERNGSLYKKSQDGIKRVWQKRCVKNGLFTTISHGTANRPPAKJNLTLTCCOVKTNP 360  
 QY 361 EEKCFDLISHDRTHYFQAEDEQECQIWMVSLQNSKEEALNNAFKGDDNTGENNIVQELT 420  
 Db 361 EEKCFDLISHDRTHYFQAEDEQECQIWMVSLQNSKEEALNNAFKGDDNTGENNIVQELT 420  
 QY 421 KEIITSEVORTGNDVCCDCCGAPDPTWLTNLGILTCIECSGIRHRELGVHYSRMOQLTLDV 480  
 Db 421 KAILGEVCRMAGNDVCCDCCGAPDPTWLTNLGILTCIECSGIRHRELGVHYSRMOQLTLDV 480

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: April 18, 2005, 18:42:21 ; Search time 87.3111 Seconds  
(without alignments)  
4456.258 Million cell updates/sec

Title: US-09-914-042-1  
Perfect score: 5273  
Sequence: 1 MPDQISVSEFVAETHDYKA.....DGDPCRGAFFVSVFHFAD 1006

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:.\*  
1: Geneseq1980s:.\*  
2: Geneseq1990s:.\*  
3: Geneseq2000s:.\*  
4: Geneseq2001s:.\*  
5: Geneseq2002s:.\*  
6: Geneseq2003as:.\*  
7: Geneseq2003bs:.\*  
8: Geneseq2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5253	99.6	1006	2	AAW77290	AAW77290 Human dif
2	5084	96.4	1006	3	AAW223647	AAW223647 Human Pap
3	3874	73.5	982	2	AAW77288	AAW77288 Zebrafish
4	3710.5	70.4	783	3	AAW23648	AAW23648 Murine Pa
5	3155	59.8	903	2	AAW77289	AAW77289 Zebrafish
6	3029	57.4	1072	7	ADD71162	ADD71162 Human int
7	3024.5	57.4	1129	7	ADD71155	ADD71155 Human int
8	3013.5	57.1	1129	2	AAW77286	AAW77286 Bovine di
9	3011	57.1	1090	6	AAE38437	AAE38437 Mouse ASA
10	3006	57.0	1132	8	ADJ51009	ADJ51009 Human nov
11	3000.5	56.9	1147	6	AAE38436	AAE38436 Mouse ASA
12	2954.5	56.0	1151	2	AAW77287	AAW77287 Zebrafish
13	2852	54.1	1087	8	ADS34461	ADS34461 POSH prot
14	2465.5	46.8	956	8	ADS34457	ADS34457 POSH prot
15	2410	45.7	949	8	ADS34458	ADS34458 POSH prot
16	2369	44.9	940	8	ADS10772	ADS10772 Human the
17	2363	44.8	940	4	AAW40068	AAW40068 Human pol
18	2071.5	39.3	903	7	ADB64797	ADB64797 Human pro
19	2071.5	39.3	903	7	ADK81947	ADK81947 Hepatocel
20	1801.5	34.2	350	4	AAU87117	AAU87117 Novel cen
21	1801.5	34.2	350	8	ADI54432	ADI54432 Novel hum
22	1759.5	33.4	349	4	AAU87438	AAU87438 Novel cen
23	1759.5	33.4	349	8	ADI54753	ADI54753 Novel hum
24	1695.5	32.2	1020	4	ABD58971	ABD58971 Drosophil
25	1075.5	20.4	208	7	ABD64130	ABD64130 Human pro

26	802	15.2	459	4	AAU20370	AAU20370 Human sec
27	611.5	11.6	358	7	ADJ71009	ADJ71009 Human bea
28	579	11.0	407	5	ABW97460	ABW97460 Novel hum
29	573.5	10.9	778	7	ADD71161	ADD71161 Human int
30	571.5	10.8	778	4	AAW39122	AAW39122 Human pol
31	569	10.8	407	6	ABU70671	ABU70671 Human adi
32	562	10.7	799	4	ABG17242	ABG17242 Novel hum
33	558	10.6	764	6	ABU52617	ABU52617 Human NOV
34	551	10.4	804	5	ABB97954	ABB97954 Human pro
35	532.5	10.1	805	4	AAW40908	AAW40908 Human pol
36	530.5	10.1	958	8	ADS10512	ADS10512 Human the
37	529	10.0	834	5	ABG91802	ABG91802 Human int
38	529	10.0	834	5	AAU99904	AAU99904 Human 468
39	509	9.7	740	8	ADS34455	ADS34455 POSH prot
40	480	9.1	156	4	ABB11268	ABB11268 Human dif
41	439	8.3	828	4	ABB62649	ABB62649 Drosophil
42	422.5	8.0	560	4	AAE07122	AAE07122 Human gen
43	419	7.9	605	5	ABG93808	ABG93808 Transcrip
44	419	7.9	605	5	AAU71799	AAU71799 Zinc fing
45	412	7.8	176	4	AAW41854	AAW41854 Human pol

ALIGNMENTS

RESULT 1  
AAW77290  
ID AAW77290 standard; protein; 1006 AA.  
XX  
AC AAW77290;  
XX  
DT 20-NOV-1998 (first entry)  
XX  
DE Human differentiation enhancing factor 2 gene.  
XX  
KW Human; differentiation enhancing factor; ankyrin repeat; C2 domain;  
KW SH3 consensus binding sequence; pleckstrin homology domain; adipogenesis;  
KW neurogenesis; hyperplastic disease; neoplastic disease; nervous system.  
XX  
OS Homo sapiens.  
XX  
PN WO9836065-A1.  
XX  
PD 20-AUG-1998.  
XX  
PF 13-FEB-1998; 98WO-US002724.  
XX  
PR 14-FEB-1997; 97US-0038191P.  
XX  
PI (DAND) DANA FARBER CANCER INST INC.  
XX  
PI Thomas RM, King FJ, Harris DF, Hu E, Spiegelman B, Chan J;  
XX  
WPI; 1998-467173/40.

Exhibit A

New nucleic acid encoding differentiation enhancing factor - used particularly to regulate adipogenesis and neurogenesis, e.g. for treating tumours and neurological disease.  
Example 13; Fig 12; 203pp; English.

The differentiation enhancing factors (DEF), comprise at least one each of SH3 consensus binding sequence, ankyrin repeat, pleckstrin homology domain and C2 domain. The DEF induce adipogenesis or neurogenesis; they are mediators of SH3-domain dependent signalling and may be involved in cellular gene expression, cytoskeletal architecture, protein trafficking, endocytosis or adhesion, migration, proliferation and differentiation of cells. Typical applications of DEF and agents that modulate interaction between the protein and it's ligand, or of nucleic acid expressing them, are treatment of hyperplastic and neoplastic disease (a wide range of solid tumours and leukaemias), including metastases; for in vitro induction of differentiation of neural crest cells to neurons, glial cells etc.; for increasing neuron survival, and inducing cell repair, in

CC the nervous system (e.g. treatment of traumatic injury, stroke,  
 CC Alzheimer's, Parkinson's or Huntington's diseases, amyotrophic lateral  
 CC sclerosis, multiple sclerosis etc.)  
 XX Sequence 1006 AA;

Query Match  
 Best Local Similarity 99.6%; Score 5253; DB 2; Length 1006;  
 Matches 1003; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPQISVSFVAETHEDYKAPTASSFTTRTAQCRNTVAALAEALDVRMVLKMKSVKA 60  
 Db 1 MPQISVSFVAETHEDYKAPTASSFTTRTAQCRNTVAALAEALDVRMVLKMKSVKA 60  
 Qy 61 INSSGLAHVENEEOYTOALEKFGNCVCRDDPDLSAFLKFSVFTKELTALFKNLQNN 120  
 Db 61 INSSGLAHVENEEOYTOALEKFGNCVCRDDPDLSAFLKFSVFTKELTALFKNLQNN 120  
 Qy 121 NIISFPLDLSLLKGDVGKDLKPKFDKAWDYETKITKEKEKSHAKLHGMIRTEISG 180  
 Db 121 NIISFPLDLSLLKGDVGKDLKPKFDKAWDYETKITKEKEKSHAKLHGMIRTEISG 180  
 Qy 181 ASIAEMEKEKRRFFOLQMCCEYLLKNEIKIKGVLDLQNLKIFYHAQCNFFODGLKAVES 240  
 Db 181 ASIAEMEKEKRRFFOLQMCCEYLLKNEIKIKGVLDLQNLKIFYHAQCNFFODGLKAVES 240  
 Qy 241 LKPSIETLSTDLHTTKQAQDEERRQIOLRDILKSALQVEKEDSQIRQSTAYSILHQPQ 300  
 Db 241 LKPSIETLSTDLHTTKQAQDEERRQIOLRDILKSALQVEKEDSQIRQSTAYSILHQPQ 300  
 Qy 301 NKEHGTENGSLYKSDGIRKWKRCVKNGLTISHGTANRPAPKLNLLTCQVKNP 360  
 Db 301 NKEHGTENGSLYKSDGIRKWKRCVKNGLTISHGTANRPAPKLNLLTCQVKNP 360  
 Qy 361 EEKCFDLISHDRTHYFOAEDEQECQIWMVLSQNSKEALNNAFKGDDNTGENNIVBELT 420  
 Db 361 EEKCFDLISHDRTHYFOAEDEQECQIWMVLSQNSKEALNNAFKGDDNTGENNIVBELT 420  
 Qy 421 KEIISEVQRTGNDVCCGAPDPTLSTNLGILTCIECSIHRELGVHSPQMSLTLDV 480  
 Db 421 KEIISEVQRTGNDVCCGAPDPTLSTNLGILTCIECSIHRELGVHSPQMSLTLDV 480  
 Qy 481 LGTSELLAKNIGNAGFNEIMECCLPAEDSVKPNPGSDMNARKDYITAKVIERARYKXH 540  
 Db 481 LGTSELLAKNIGNAGFNEIMECCLPAEDSVKPNPGSDMNARKDYITAKVIERARYKXH 540  
 Qy 541 ADNAKLHSLCEAVKTRDIFGLLOAYADGVDLTEKPLANGHEPDTALHLAVRSVDRTS 600  
 Db 541 ADNAKLHSLCEAVKTRDIFGLLOAYADGVDLTEKPLANGHEPDTALHLAVRSVDRTS 600  
 Qy 601 LHVDPLVQNSGLDKQTKGSTALHYCCLTDAECLKLLRGKASIRIANESGETPLDI 660  
 Db 601 LHVDPLVQNSGLDKQTKGSTALHYCCLTDAECLKLLRGKASIRIANESGETPLDI 660  
 Qy 661 AKRLKHECEELLTQALSGRNSHVHVEYEWRLHEDLDESDDMDKLOPSENERDRP 720  
 Db 661 AKRLKHECEELLTQALSGRNSHVHVEYEWRLHEDLDESDDMDKLOPSENERDRP 720  
 Qy 721 ISFYOLGNSQLQSNVSLARDAANLAKKORAFMPSILQNETYCALLSGSPPPAQAAPS 780  
 Db 721 ISFYOLGNSQLQSNVSLARDAANLAKKORAFMPSILQNETYCALLSGSPPPAQAAPS 780  
 Qy 781 TTSAPPLPPRVNGKVQTASSANTLWKTNSVSDGSRQRSSDDPAPHPLPLPLRVSTN 840  
 Db 781 TTSAPPLPPRVNGKVQTASSANTLWKTNSVSDGSRQRSSDDPAPHPLPLPLRVSTN 840  
 Qy 841 PLTPTPPPPVAKTPSWNEALSQPSKAPPGISQIRPPPLPPQPSRLPOKKPARGTDKST 900  
 Db 841 PLTPTPPPPVAKTPSWNEALSQPSKAPPGISQIRPPPLPPQPSRLPOKKPARGTDKST 900  
 Qy 901 PLTNKQPPGPDLSATEALGPLSNAMVLOPPAMPKRSQATKLKPKRVKALYNCVADNP 960  
 Db 901 PLTNKQPPGPDLSATEALGPLSNAMVLOPPAMPKRSQATKLKPKRVKALYNCVADNP 960

Qy 961 DELTFSEGDVIIVDGEEDQEWIIGHIDGIDPCRKGAPVSVFHFITAD 1006  
 Db 961 DELTFSEGDVIIVDGEEDQEWIIGHIDGIDPCRKGAPVSVFHFITAD 1006

RESULT 2  
 AAB23647  
 ID AAB23647 standard; protein; 1006 AA.  
 XX AAB23647;  
 XX AAB23647;  
 DT 05-JAN-2001 (first entry)  
 XX Human Pap-DELTA protein sequence SEQ ID NO:1.

KW Pap; Pyk2 binding protein; Pyk2 C-terminus associated protein; diagnosis;  
 KW cytosolic; neuroprotective; immunomodulatory; cardioactive; cancer;  
 KW cardiovascular disorder; neurodegenerative disorder; immune disorder.

OS Homo sapiens.

XX WO200049144-A2.  
 XX 24-AUG-2000.

XX 18-FEB-2000; 2000WO-US004647.  
 XX 22-FEB-1999; 99US-0121125P.

XX (SUGEN-) SUGEN INC.

XX Lev S, Schlessinger J, Chen A, Hernandez J, Martinez R;  
 XX Plowman GD;

XX WPI; 2000-524592/47.

XX Pyk2 binding protein nucleic acids, polypeptides, antibodies and  
 XX antisense oligonucleotides, the oligonucleotides are useful for treating  
 XX cancer or a cardiovascular, neurodegenerative or immune disorder.  
 XX Claim 15; Fig 1; 132pp; English.

XX The present sequence represents the human Pap-DELTA protein. Pap is a  
 XX Pyk2 C-terminal associated protein (Pyk2 binding protein). Pap proteins  
 XX have cytostatic, neuroprotective, immunomodulatory and cardioactive  
 XX activities. Pyk2 binding protein, immunomodulatory and cardioactive  
 XX diagnostic agents for the detection of diseases. Oligonucleotides from  
 XX polynucleotide sequences encoding Pap proteins may be useful for the  
 XX treatment of diseases such as cancer or a cardiovascular,  
 XX neurodegenerative or immune disorder

XX Sequence 1006 AA;

Query Match  
 Best Local Similarity 96.4%; Score 5084; DB 3; Length 1006;  
 Matches 983; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 1 MPQISVSFVAETHEDYKAPTASSFTTRTAQCRNTVAALAEALDVRMVLKMKSVKA 60  
 Db 1 MPQISVSFVAETHEDYKAPTASSFTTRTAQCRNTVAALAEALDVRMVLKMKSVKA 60  
 Qy 61 INSSGLAHVENEEOYTOALEKFGNCVCRDDPDLSAFLKFSVFTKELTALFKNLQNN 120  
 Db 61 INSSGLAHVENEEOYTOALEKFGNCVCRDDPDLSAFLKFSVFTKELTALFKNLQNN 120  
 Qy 121 NIISFPLDLSLLKGDVGKDLKPKFDKAWDYETKITKEKEKSHAKLHGMIRTEISG 180  
 Db 121 NIISFPLDLSLLKGDVGKDLKPKFDKAWDYETKITKEKEKSHAKLHGMIRTEISG 180  
 Qy 181 ASIAEMEKEKRRFFOLQMCCEYLLKNEIKIKGVLDLQNLKIFYHAQCNFFODGLKAVES 240  
 Db 181 ASIAEMEKEKRRFFOLQMCCEYLLKNEIKIKGVLDLQNLKIFYHAQCNFFODGLKAVES 240

QY	241	LKPSIETLSLTLHTIKQAQDEERRQLIQLRDLKSAQVQKEDSQIRQSTAYSLHQPOG	300
Db	241	LKPSIETLSLTLHTIKQAQDEERRQLIQLRDLKSAQVQKEDSQIRQSTAYSLHQPOG	300
QY	301	NKEHGTGRNSLYKSGDGIKRWKRCVKNGLTISHGTANRPPAKNLTLCOVKTNP	360
Db	301	NKEHGTGRNSLYKSGDGIKRWKRCVKNGLTISHGTANRPPAKNLTLCOVKTNP	360
QY	361	EEKKCFDLISHDRTHYFQAEDQECQIWMVSLQNSKEEALNNAFKGDDNTGNNIVQELT	420
Db	361	EEKKCFDLISHDRTHYFQAEDQECQIWMVSLQNSKEEALNNAFKGDDNTGNNIVQELT	420
QY	421	KEIISVQRTMGNDVCCGAPDPTWLSNLGILTCIECSGIRHGLVHVSQMSLTLDV	480
Db	421	KEIISVQRTMGNDVCCGAPDPTWLSNLGILTCIECSGIRHGLVHVSQMSLTLDV	480
QY	481	LGTSELLAKNIGNAGNETWECCLPADSVKPNFGSDMNAKDYITAKYIERRYARKKH	540
Db	481	LGTSELLAKNIGNAGNETWECCLPADSVKPNFGSDMNAKDYITAKYIERRYARKKH	540
QY	541	ADNAAKLHSLCEAVKTRDIFGLLOAVADGVDLTEKIFLANGHEPDETALHLAVRSVDRTS	600
Db	541	ADNAAKLHSLCEAVKTRDIFGLLOAVADGVDLTEKIFLANGHEPDETALHLAVRSVDRTS	600
QY	601	LHIVDFLVQNSGMLDKQTKGKSTALHYCCLTDAECLKLLRGKASIEIANESGETPLDI	660
Db	601	LHIVDFLVQNSGMLDKQTKGKSTALHYCCLTDAECLKLLRGKASIEIANESGETPLDI	660
QY	661	AKRLKHEHCELLTOALSGRFSNVHVEYWRLLHEDLDESDDDMDKLOPSENREDRP	720
Db	661	AKRLKHEHCELLTOALSGRFSNVHVEYWRLLHEDLDESDDDMDKLOPSENREDRP	720
QY	721	ISFYQLGSLQNSLQNAVSLARDAANLAKEKORAFMPSILQNETYCALLSGSPPPAQAAPS	780
Db	721	ISFYQLGSLQNSLQNAVSLARDAANLAKEKORAFMPSILQNETYCALLSGSPPPAQAAPS	780
QY	781	TTSAAPLPVRNVGKVQTASSANTLWKTNSVSDGGRSQRSSDPPAVHPLPLRVSTN	840
Db	781	TTSAAPLPVRNVGKVQTASSANTLWKTNSVSDGGRSQRSSDPPAVHPLPLRVSTN	840
QY	841	PLTPTPPPPVAKTPSWEALSQSKPAPPGISQIRPPPLPPQPPSRLPQKKPAPGTDKST	900
Db	841	PLTPTPPPPVAKTPSWEALSQSKPAPPGISQIRPPPLPPQPPSRLPQKKPAPGTDKST	900
QY	901	PLTNKGOPRGPVDSLATEALGPLSNAMVLOPPAPMPRKSOATKLKPRVKALYNCVADNP	960
Db	901	PLTNKGOPRGPVDSLATEALGPLSNAMVLOPPAPMPRKSOATKLKPRVKALYNCVADNP	960
QY	961	DELTFSEGDIIVDGEEDQEWIGHIDGDPGRKGAFFVSVFHIAD	1006
Db	961	DELTFSEGDIIVDGEEDQEWIGHIDGDPGRKGAFFVSVFHIAD	1006
RESULT 3			
AAW77288			
ID	AAW77288	standard; protein; 982 AA.	
XX			
AC	AAW77288;		
XX			
DT	17-OCT-2003 (revised)		
DT	20-NOV-1998 (first entry)		
XX			
DE	Zebrafish differentiation enhancing factor 2 protein.		
XX			
KW	Zebrafish; differentiation enhancing factor; ankyrin repeat; C2 domain;		
KW	SH3 consensus binding sequence; pleckstrin homology domain; adipogenesis;		
KW	neurogenesis; hyperplastic disease; neoplastic disease; nervous system.		
XX			
OS	Danio rerio.		
XX			
PN	W09836065-A1.		
XX			

PD	20-AUG-1998.		
XX			
PF	13-FEB-1998; 98WO-US002724.		
PR			
XX	14-FEB-1997; 97US-0038191P.		
XX			
PA	(DAND ) DANA FARBER CANCER INST INC.		
XX			
PI	Thomas RM, King FJ, Harris DF, Hu E, Spiegelman B, Chan J;		
XX			
DR	WPI; 1998-467173/40.		
DR	N-PSDB; AAV59105.		
XX			
PT	New nucleic acid encoding differentiation enhancing factor - used		
PT	particularly to regulate adipogenesis and neurogenesis, e.g. for treating		
PT	tumours and neurological disease.		
XX			
PS	Claim 3; Fig 12; 203pp; English.		
XX			
CC	The differentiation enhancing factors (DEF), comprise at least one each		
CC	of SH3 consensus binding sequence, ankyrin repeat, pleckstrin homology		
CC	domain and C2 domain. The DEF induce adipogenesis or neurogenesis; they		
CC	are mediators of SH3-domain dependent signalling and may be involved in		
CC	cellular gene expression, cytoskeletal architecture, protein trafficking,		
CC	endocytosis or adhesion, migration, proliferation and differentiation of		
CC	cells. Typical applications of DEF and agents that modulate interaction of		
CC	between the protein and it's ligand, or of nucleic acid expressing them,		
CC	are treatment of hyperplastic and neoplastic disease (a wide range of		
CC	solid tumours and leukaemias), including metastases; for in vitro		
CC	induction of differentiation of neural crest cells to neurons, glial		
CC	cells etc.; for increasing neuron survival, and inducing cell repair, in		
CC	the nervous system (e.g. treatment of traumatic injury, stroke,		
CC	Alzheimer's, Parkinson's or Huntington's diseases, amyotrophic lateral		
CC	sclerosis, multiple sclerosis etc.). (Updated on 17-OCT-2003 to		
CC	standardise OS field)		
XX			
SQ	Sequence 982 AA;		
	Query Match 73.5%; Score 3874; DB 2; Length 982;		
	Best Local Similarity 74.1%; Pred. No. 6.4e-264;		
	Matches 755; Conservative 92; Mismatches 122; Indels 50; Gaps 13;		
QY	1 MPDQISVSFFVAETHEDYKAPTASSFTTTRTAOCRNTVAAIEEALDVRMVLKMKKSVKA	60	
Db	1 MPDQITVAEFVTETNEDYKSPASFTTTRMTWTHCRNTVSALEBALDVRSLVKMKKSVKA	60	
QY	61 INSSGLAHVENEEOYTOALEKFGGNCVCRDDPDLSAFLKFSVFTKLTALFKNLQNN	120	
Db	61 IYASGLAHVENEEOYTOALEKFGGNCVCRDDPDLSAFLKFSVFTKLTALFKNLQNN	120	
QY	121 NIISFPLDLSLLKGLDKGVKGLKPKDPKAWKDYETKITKEKEKHAHLGHMIRTEISG	180	
Db	121 NIITFPLDLSLLKGLDKGVKGLKPKDPKAWKDYETKITKEKEKHAHLGHMIRTEISG	180	
QY	181 ABIAEMEKEKRRFFOLQMCCEYLLKVNIEIKIKGVLDLQNLIKYFHAQCNFFQDGLKAVES	240	
Db	181 ABIAEMEKEKRRFFOLQMCCEYLLKVNIEIKIKGVLDLQNLIKYFHAQCNFFQDGLKAVDN	240	
QY	241 LKPSITLSTDLHTIKQAQDEERRQLIQLRDLKSAQVQKEDSQIRQSTAYSLHQPOG	300	
Db	241 LKPSIEKLATDLHSIKQVQDEERRQLIQLRDLKSAQVQKEDSQIRQSTAYSLHQPOG	300	
QY	301 NKEHGTGRNSLYKSGDGIKRWKRCVKNGLTISHGTANRPPAKNLTLCOVKTNP	360	
Db	301 NKEHGTGRNSLYKSGDGIKRWKRCVKNGLTISHGTANRPPAKNLTLCOVKTNP	360	
QY	361 BEKKCFDLISHDRTHYFQAEDQECQIWMVSLQNSKEEALNNAFKGDDNTGNNIVQELT	420	
Db	361 BEKKCFDLISHDRTHYFQAEDQECQIWMVSLQNSKEEALNNAFKGDDNTGNNIVQELT	420	
QY	421 KEIISVQRTMGNDVCCGAPDPTWLSNLGILTCIECSGIRHGLVHVSQMSLTLDV	480	
Db	421 KAILGEVCRMAGNDVCCGAPDPTWLSNLGILTCIECSGIRHGLVHVSQMSLTLDV	480	